Attorney Docket No.: **DEX-0054**
Inventors: **Robbins et al.**
Serial No.: **09/426,548**
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REMARKS

Claims 2, 3 and 9 are pending in the instant application. Claims 2, 3 and 9 have been rejected. Claims 2, 3 and 9 have been amended. Support for amendments to the claims can be found in the specification at pages 16, line 15 through page 17, line 16, page 17, line 34 through page 18, line 26, and page 18, line 32 through page 20, line 5. No new matter has been added by these amendments. Reconsideration is respectfully requested in light of these amendments and the following remarks.

I. Rejection of Claims 2, 3 and 9 under 35 U.S.C. 112, second paragraph

Claims 2, 3 and 9 have been rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. Specifically, the Examiner suggests that claim 9 is vague and indefinite for the recitation of an "oligonucleotide probe hybridizing" because the specification conditions for hybridization are not clearly set forth in the claim or defined in the specification.

Accordingly, in an earnest effort to advance the

prosecution of this case, but without conceding in any way to the Examiner's suggestion, Applicants have amended claim 9 to remove this phrase.

Withdrawal of this rejection under 35 U.S.C. 112, second paragraph, is therefore respectfully requested.

II. Rejection of Claims 2, 3 and 9 under 35 U.S.C. 102(b) and 102(e)

The rejections of claims 2, 3 and 9 under 35 U.S.C. 102(b) as being anticipated by Weber et al. and under 35 U.S.C. 102(e) as being anticipated by Liskay et al. have been maintained. The Examiner suggests that since the metes and bounds of claim 9 can vary and claims 2 and 3 encompass a method of screening the DNA samples which does not involve specifically screening for specific mutations, the teachings of Weber et al. and Liskay et al. relating to a method and primers for genomic sequencing of MLH1 and MSH2 to detect mutations predictive of heredity non-polyposis colorectal cancer anticipates the claims.

Applicants respectfully traverse this rejection.

As discussed in previous responses, the teachings of Weber et al. and Liskay et al. are not related to detection of all of the same mutations taught in the instant invention

and the oligonucleotide probes used in the methods of claim 2 and 3 are complementary to mutants other than those taught by Weber et al. and Liskay et al. In an earnest effort to more clearly distinguish the instant invention from the teachings of Weber et al. and Liskay et al., however, Applicants have amended claims 2 and 3 to specifically state those mutants detected in the present invention. Support for this amendment can be found in the specification at pages 16, line 15 through page 17, line 16, page 17, line 34 through page 18, line 26, and page 18, line 32 through page 20, line 5 wherein methods for detecting these mutants with oligonucleotide probes to diagnosis HNPCC in a patient and determine the susceptibility of a patient for developing HNPCC are specifically set forth. Since neither Weber et al. nor Liskay et al. teaches detection of these mutants to diagnose HNPCC and predict susceptibility of a patient to HNPCC, these references cannot anticipate the claims as amended.

Withdrawal of these rejections under 35 U.S.C. 102(b) and 35 U.S.C. 102(e) is therefore respectfully requested.

III. Conclusion

Applicants believe the foregoing comprises a full and complete response to the Office Action of record. Accordingly, favorable reconsideration and subsequent allowance of the pending claims is earnestly solicited.

Attached hereto is a marked-up version of the changes made to the specification and claims by the current amendment. The attached page is captioned "Version with Markings to Show Changes Made."

Respectfully submitted,

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Claims:

Claims 2, 3 and 9 have been amended as follows:

2. (amended) A method of diagnosing hereditary non-polyposis colorectal cancer in a patient comprising:

(a) obtaining a DNA or RNA sample from a patient; and

(b) screening the DNA or RNA sample with the oligonucleotide probe of claim 9 to detect a hMLH1 mutant 1, a hMSH2 mutant 1, a hMSH2 mutant 2, or a hMSH2 mutant 3, wherein binding of the oligonucleotide probe to the DNA or RNA sample is indicative of the presence of the hMLH1 mutant 1, the hMSH2 mutant 1, the hMSH2 mutant 2, or the hMSH2 mutant 3 and hereditary non-polyposis colorectal cancer.

3. (amended) A method for predicting susceptibility of a patient to developing hereditary non-polyposis colorectal cancer comprising:

(a) obtaining a DNA or RNA sample from a patient; and

(b) screening the DNA or RNA sample with the oligonucleotide probe of claim 9 to detect a hMLH1 mutant 1, a hMSH2 mutant 1, a hMSH2 mutant 2, or a hMSH2 mutant 3, wherein binding of the oligonucleotide probe to the DNA or RNA sample is indicative of the presence of the hMLH1 mutant

1, the hMSH2 mutant 1, the hMSH2 mutant 2, or the hMSH2 mutant 3 and hereditary non-polyposis colorectal cancer.

9. (amended) An oligonucleotide probe complementary to a hMLH1 mutant 1, hMSH2 mutant 1, hMSH2 mutant 2, or hMSH2 mutant 3~~, said oligonucleotide probe hybridizing to hMLH1 mutant 1, hMSH2 mutant 1, hMSH2 mutant 2, or hMSH2 mutant 3~~.